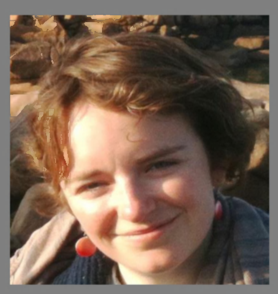
Assessing connectivity in young flatfish and its implementation in fisheries management



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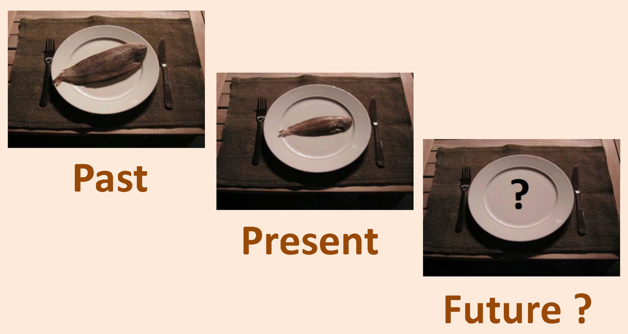
INTRODUCTION & AIMS



- **Overfishing and selective fishing** lead to a loss of genetic diversity as well as changed life cycles. Given the commercial importance of the North Sea sole species, **conservation efforts** have to be made.
- **Interannual variability in recruitment*** (Fig. 1) and dispersal (Fig. 4) remain poorly explained. However **sustainable stock* management** requires an upgraded biological assessment of population structure and connectivity patterns.
- **Early life stages** are of critical importance for recruitment and they provide a unique opportunity to **reveal connectivity patterns**.

Interannual recruitment variability

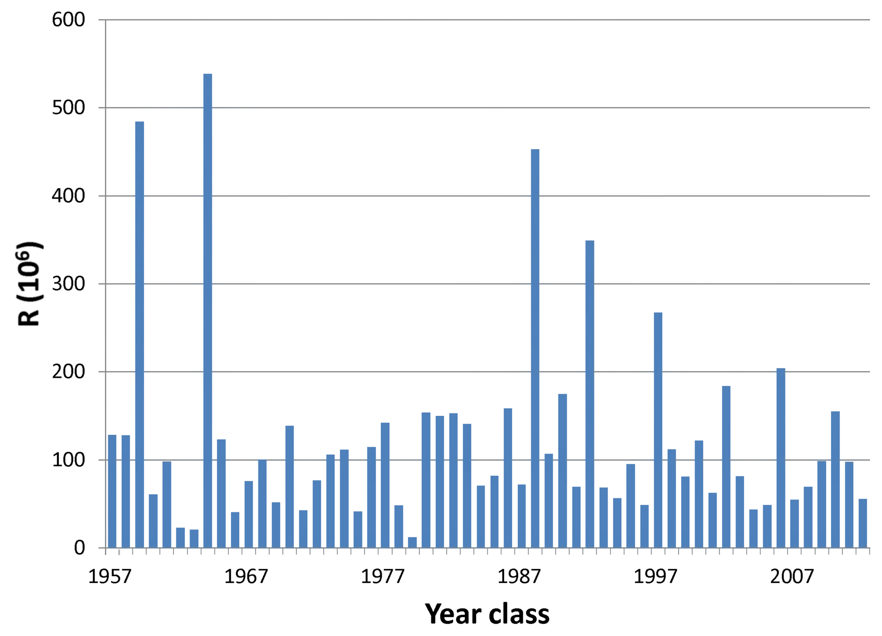


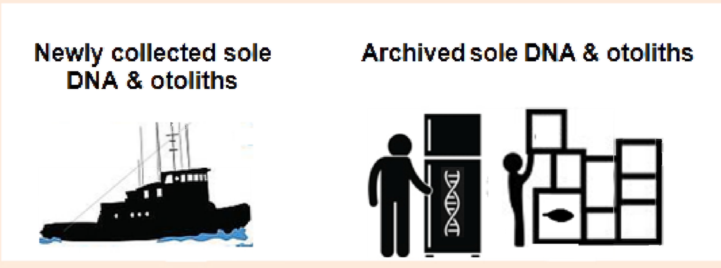
Figure 1: Recruitment (R) variability in the North Sea sole (ICES 2013).

OBJECTIVES

1. Does larval dispersal vary in time and space?
2. What biotic and abiotic factors are driving larval connectivity?
3. Can we predict the impact on recruitment of changes in physical and biological drivers?

STUDY AREA

(1) TEMPORAL SAMPLING
Years 2013 & 2014 + Archives 1975-2008



(2) SPATIAL SAMPLING

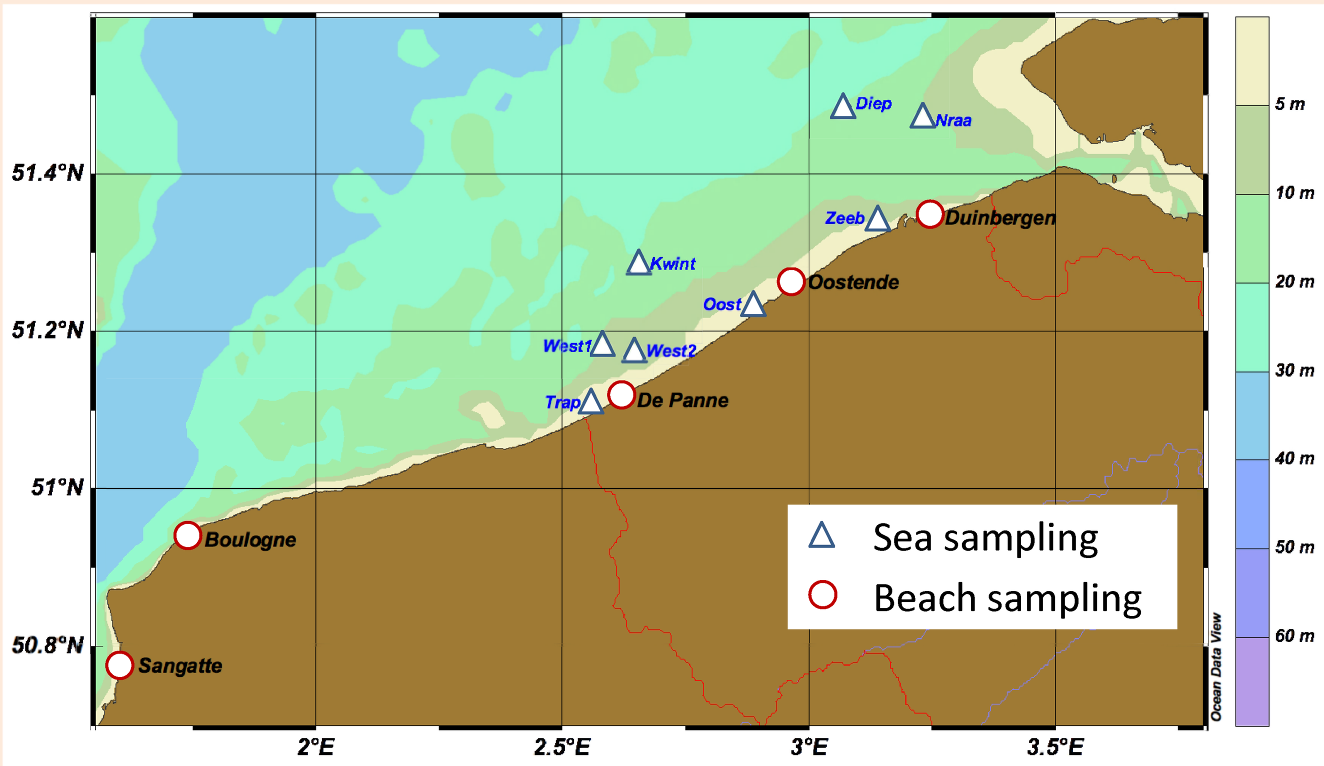


Figure 2: Sampling points of sole larvae, postlarvae and juveniles along the Belgian-French coast. Sea sampling = beam trawl, benthic sledge and WP3 plankton net. Beach sampling = beam trawl on foot. Fish size limit <10cm. Courtesy of A. Vanden Bavière.

METHODOLOGY

(1) ENVIRONMENTAL CHEMICAL HETEROGENEITY

Tool 1: Microchemistry: Otolith elemental composition

15 chemical elements (e.g., Na, Ba, Mn)

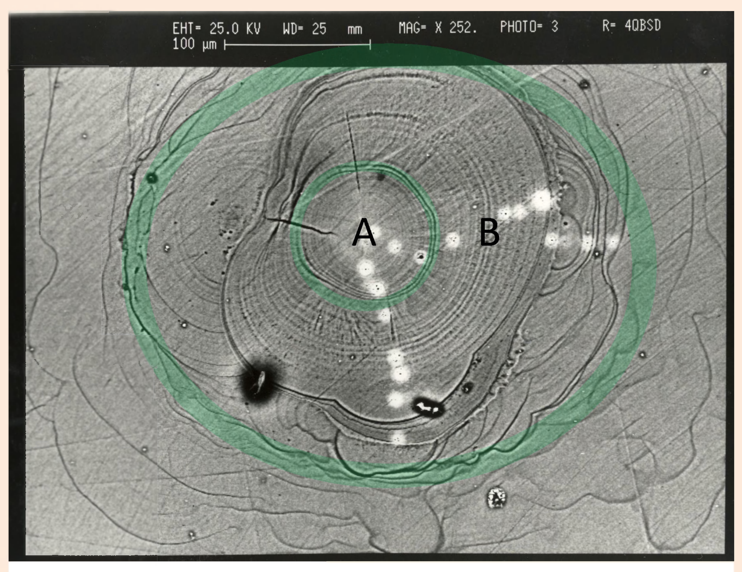


Figure 3: Sole postlarval otolith sampled for ICPMS.
A: natal signature (core of the otolith).
B: capture location signature (edge).
Sample holes in white.
Courtesy of A. Gueffen.

(2) LOCAL GENETIC SIGNATURE

Tool 2: SNPs for sole

Screen FishPopTrace's 426 SNPs* for 4 Atlantic populations

↓ Illumina-Veracode Genotyping

↓ 200 outlier SNPs

↓ Connectivity matrix

Origin assignment

↓ Correlation analysis between matrices

↓ Temporal stability analysis between old and new samples

Seascape (spatial) analysis

↓ Population structure, relatedness and population origin

SCENARIO TESTING – IPCC PREDICTIONS

- River runoff, SST, wind & atmospheric pressure, behaviour
- Larval retention (Fig. 4)

Tool 3: Modelling of larval dispersal

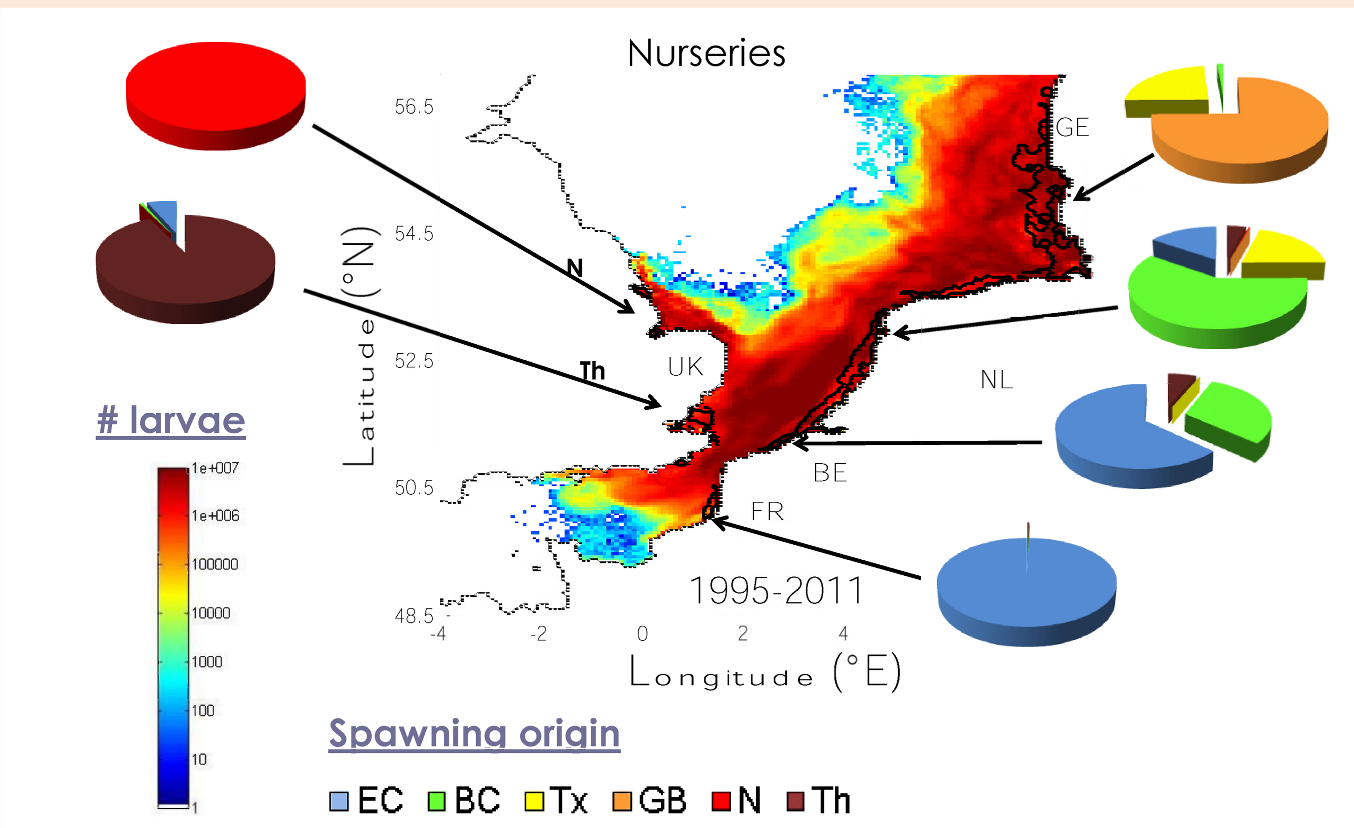


Figure 4: Larval abundance of North Sea sole at the end of larval transport obtained from a bio-hydrodynamic model (Lacroix et al. 2013).
Relative contributions of 6 spawning grounds: EC (Eastern English Channel), BC (off the Belgian coast), Tx (off Texel), GB (inner German Bight), N (Norfolk banks), Th (Thames estuary).

OUTCOMES

- **Individual tracing** with otolith microchemistry and genomics to understand:
  - → dispersal and connectivity
  - → recruitment
- Comparison of **bio-hydrodynamic model** with ***in situ* data**
  - → to assess the relative impacts of hydrodynamics, environment, behaviour and physiology
  - → to improve the predictability of **cohort strength**
- Fisheries **management** at the subpopulation level because of:
  - → potential collapse of less productive components
  - → the importance of biocomplexity for long term stability and **sustainability of fish stocks**

VOCABULARY

* **Recruitment:** the part of fish juveniles that have reached a sufficient length to enter the stock
SNPs: Single Nucleotide Polymorphisms are molecular markers
Stock: the economically exploitable part of a population

BIBLIOGRAPHY

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ICES Advice 2013, Book 6 – http://www.ices.dk/sites/pub/Publication%20Reports/Advice/2013/2013/sol-nsea.pdf

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FWO – Project nr G.0702.13N (2013-2016) *"Understanding and predicting the impact of the interaction between oceanographic and biological factors on larval recruitment and population connectivity in flatfish – B-FishConnect".*

Old datasets: Beyst et al. 2001,2002; Cuveliers et al. 2010; Dewicke et al. 2003; Rogers et al. 1998; Van der Veer et al. 2011.